

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1 - 5. (Canceled)

6. (Currently amended) The method of claim 8, wherein the DNA methylation pattern for the test ~~stem-cell~~, test ~~stem-cell~~-tissue, or test ~~stem-cell~~-nucleus and the differentiation state-specific DNA methylation pattern each comprise information on the methylation state of at least about 1,000 gene regions.

7. (Canceled)

8. (Currently amended) A method of identifying the differentiation state of a test ~~stem-cell~~, test ~~stem-cell~~-tissue, or test ~~stem-cell~~-nucleus, wherein the test cell, test tissue, or test nucleus is selected from a stem cell, a stem cell tissue, a stem cell nucleus, a differentiating stem cell, a differentiating stem cell tissue, a differentiating stem cell nucleus, a cell differentiated from a stem cell, a tissue differentiated from a stem cell tissue, and a nucleus differentiated from a stem cell nucleus comprising:

obtaining a DNA methylation pattern for the test ~~stem-cell~~, test ~~stem-cell~~-tissue, or test ~~stem-cell~~-nucleus, wherein the DNA methylation pattern for the test ~~stem-cell~~, test ~~stem-cell~~-tissue, or test ~~stem-cell~~-nucleus comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a differentiation state-specific DNA methylation pattern for one or more ~~stem-cell~~, ~~stem-cell~~-tissue, or ~~stem-cell~~-nucleus of known differentiation state, wherein the one or more cell, tissue, or nucleus of known differentiation state is selected from a stem cell, a stem cell tissue, a stem cell nucleus, a differentiating stem cell, a differentiating stem cell tissue, a differentiating stem cell nucleus, a cell differentiated from a stem cell, a tissue differentiated from a stem cell tissue, and a nucleus differentiated from a stem cell nucleus; and,

comparing the DNA methylation pattern for the test ~~stem-cell~~, test ~~stem-cell~~-tissue, or test ~~stem-cell~~-nucleus with the differentiation state-specific DNA methylation pattern,

wherein the differentiation state of the test ~~stem-cell~~, test ~~stem-cell~~-tissue, or test ~~stem-cell~~-nucleus is identified if the DNA methylation pattern of the test ~~stem-cell~~, test ~~stem-cell~~-tissue, or test ~~stem-cell~~-nucleus matches the differentiation state-specific DNA methylation pattern.

9. (Previously presented) The method of claim 8, wherein the DNA methylation patterns are obtained by generating RLGS profiles.

10 - 18. (Canceled)

19. (Currently amended) The method of claim 8, wherein the test ~~stem-cell~~, test ~~stem-cell~~-tissue, or test ~~stem-cell~~-nucleus is an embryonic stem cell, embryonic stem cell tissue, ~~or embryonic stem cell nucleus~~, differentiating embryonic stem cell, differentiating embryonic stem cell tissue, differentiating embryonic stem cell nucleus, a cell differentiated from an embryonic stem cell, a tissue differentiated from an embryonic stem cell tissue, or a nucleus differentiated from an embryonic stem cell nucleus.

20. (Currently amended) The method of claim 8, wherein the differentiation state of the one or more ~~stem-cell~~, ~~stem-cell~~-tissue, or ~~stem-cell~~-nucleus of known differentiation state is differentiated.

21. (Currently amended) The method of claim 8, wherein the differentiation state of the one or more ~~stem-cell~~, ~~stem-cell~~-tissue, or ~~stem-cell~~-nucleus of known differentiation state is undifferentiated.

22. (Currently amended) A method of identifying a test ~~stem-cell~~, test ~~stem-cell~~-tissue, or test ~~stem-cell~~-nucleus, wherein the test cell, test tissue, or test nucleus is selected from a stem cell, a stem cell tissue, a stem cell nucleus, a differentiating stem cell, a differentiating stem cell tissue, a differentiating stem

cell nucleus, a cell differentiated from a stem cell, a tissue differentiated from a stem cell tissue, and a nucleus differentiated from a stem cell nucleus, comprising:

obtaining a DNA methylation pattern for the test ~~stem-cell~~, test ~~stem-cell-tissue~~, or test ~~stem-cell-nucleus~~, wherein the DNA methylation pattern for the test ~~stem-cell~~, test ~~stem-cell-tissue~~, or test ~~stem-cell-nucleus~~ comprises information on the methylation state of CpG at a plurality of gene regions;

obtaining a cell-, tissue-, or nucleus-specific DNA methylation pattern for one or more known types of ~~stem-cell~~, ~~stem-cell-tissue~~, or ~~stem-cell-nucleus~~; wherein the one or more known types of ~~stem-cell~~, ~~stem-cell-tissue~~, or ~~stem-cell-nucleus~~ is selected from undifferentiated embryonic stem cell, ~~differentiated-differentiating~~ embryonic stem cell, cell differentiated from embryonic stem cell, undifferentiated trophoblast stem cell, ~~and-differentiated-differentiating~~ trophoblast stem cell, and cell differentiated from trophoblast stem cell; and,

comparing the DNA methylation pattern for the test ~~stem-cell~~, test ~~stem-cell-tissue~~, or test ~~stem-cell-nucleus~~ with the cell-, tissue-, or nucleus-specific DNA methylation pattern of the known ~~stem-cell~~, ~~stem-cell-tissue~~, or ~~stem-cell-nucleus~~ to permit identification of the test ~~stem-cell~~, test ~~stem-cell-tissue~~, or test ~~stem-cell-nucleus~~ as one of the known types of ~~stem-cell~~, ~~stem-cell-tissue~~, or ~~stem-cell-nucleus~~;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the undifferentiated embryonic stem cell identifies the

test ~~stem-cell~~, test ~~stem-cell-tissue~~, or test ~~stem-cell-nucleus~~ as undifferentiated embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the ~~differentiated~~ differentiating embryonic stem cell identifies the test ~~stem-cell~~, test ~~stem-cell-tissue~~, or test ~~stem-cell-nucleus~~ as ~~differentiated~~ differentiating embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the cell differentiated from embryonic stem cell identifies the test cell, test tissue, or test nucleus as differentiated from embryonic stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the undifferentiated trophoblast stem cell identifies the test ~~stem-cell~~, test ~~stem-cell-tissue~~, or test ~~stem-cell-nucleus~~ as undifferentiated trophoblast stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the ~~differentiated~~ differentiating trophoblast stem cell identifies the test ~~stem-cell~~, test ~~stem-cell-tissue~~, or test ~~stem-cell-nucleus~~ as ~~differentiated~~ differentiating trophoblast stem cell;

wherein a match to the cell-, tissue-, or nucleus-specific DNA methylation pattern of the cell differentiated from trophoblast stem cell identifies the test cell, test tissue, or test nucleus as differentiated from trophoblast stem cell.

23. (Previously presented) The method of claim 22, wherein the DNA methylation patterns are obtained by generating RLGS profiles.

24. (New) The method of claim 8, wherein the differentiation state of the one or more cell, tissue, or nucleus of known differentiation state is differentiating.